

ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTCTCGATACCGAAACCACCGGTATGAACCAGA 70

mutD

M T A M S T A I T R Q I V L D T E T T G M N Q
TTGGTGCACACTATGAAGGCCACAAGATCATGGAGATTGGTGCCTGAAAGTGGTGAACCGTCGCCTGAC 140

mutD

I G A H Y E G H K I I E I G A V E V V N R R L T
GGGCAATAACTTCCATGTTATCTAAACCCGATCGGCTGGATCCGGAAGCCTTGGCGTACATGGT 210

mutD

G N N F H V Y L K P D R L V D P E A F G V H G
ATTGCCGATGAATTGGCTCGATAAGCCCACGTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTC 280

mutD

I A D E F L L D K P T F A E V A D E F M D Y I
GCGCGCGGAGTTGGTGAATCCATAACGCAGCGTCGATATGGCTTATGGACTACGAGTTTCGTTGCT 350

mutD

R G A E L V I H N A A F D I G F M D Y E F S L L
TAAGCGCGATATTCCGAAGACCAATACTTCTGTAAGGTACCGATAGCCTTGCCTGGCGAGGAAAATG 420

mutD

K R D I P K T N T F C K V T D S L A V A R K M
TTTCCCGGTAAGCGAACAGCCTCGATGCGTTATGCTCGCTACGAAATAGATAACAGTAAACGAAACGC 490

mutD

F P G K R N S L D A L C A R Y E I D N S K R T
TGCACGGGGCATTACTCGATGCCAGATCCTGGAAAGTTATCTGGCGATGACCGGTGGTCAAACGTC 560

mutD

L H G A L L D A Q I L A E V Y L A M T G G Q T S
GATGGCTTTGGATGGAAGGAGAGACACACAGCAACAAGGTGAAGCAACAATTAGCCGATTGTACGT 630

mutD

M A F A M E G E T Q Q Q Q G E A T I Q R I V R
CAGGCAAGTAAGTTACCGCTTGTGCGACAGATGAAGAGATTGAGCTCATGAAGCCCCTCGATC 700

mutD

Q A S K L R V V F A T D E E I A A H E A R L D
TGGTGCAGAAGAAAGGCGGAAGTTGCCCTGGCGAGCATAA 741

mutD

L V Q K K G G S C L W R A .

FIGURE 1

10	20	30	40	50	60	70	
ATGAGCTATCGTATGTTGATTATCTGGTCCAAATGT	GA	CTT	TGGCCCCGGCGCCGTTTCTGTTG				Eb_429T.dna
ATGAGCTATCGTATGTTGATTATCTGGTCCAAATGT	F	A	ACTTCTTGGCCCCGGCGCCGTTTCTGTTG				Eb_GEBT.dna
80	90	100	110	120	130	140	
TGGCCAGCGCTGCCAGCTGCTGGGGTAA	AAA	AGCCCTGCTGGTGACCGATAAGGGCCTGC	GCCCAT				Eb_429T.dna
TGGCCAGCGCTGCCAGCTGCTGGGGTAA	AAA	AGCCCTGCTGGTGACCGATAAGGGCCTGC	GCCCAT				Eb_GEBT.dna
150	160	170	180	190	200	210	
TAAAGACGGTGCTGTCGATCAGACCGTGAA	GGC	ACTGAAAGCCGCCGTATTGAGGTGGTC	ATTTTCGAC				Eb_429T.dna
TAAAGACGGTGCTGTCGATCAGACCGTGAA	GGC	ACTGAAAGCCGCCGTATTGAGGTGGTC	ATTTTCGAC				Eb_GEBT.dna
220	230	240	250	260	270	280	
GGGTCGAGCGAACCGAACGACCAACGTCG	CTG	ACGGCCATGTTCCGTAAAGAGCAGTGC	G				Eb_429T.dna
GGGTCGAGCGAACCGAACGACCAACGTCG	CTG	ACGGCCATGTTCCGTAAAGAGCAGTGC	G				Eb_GEBT.dna
290	300	310	320	330	340	350	
ACATGATAATCACCGTCGGCGGGCAGCCC	G	CGACTGCGTAAAGGCATTGGTATTGCG	GGCCACCCCA				Eb_429T.dna
ACATGATAATCACCGTCGGCGGGCAGCCC	G	CGACTGCGTAAAGGCATTGGTATTGCG	GGCCACCCCA				Eb_GEBT.dna
360	370	380	390	400	410	420	
CCGGGTGATCTGTA	CAGCTATGCCGGTATCGAA	ACACTCACCAACCCGCTGCCGCC	CATTATTGCGGT				Eb_429T.dna
CCGGGTGATCTGTA	CAGCTATGCCGGTATCGAA	ACACTCACCAACCCGCTGCCGCC	CATTATTGCGGT				Eb_GEBT.dna
430	440	450	460	470	480	490	
AAACACCACCGCCGGGACC	GCGAACG	AGTCACCCGCCACTGCGTGCTGACT	AAACACCAAAACCAAAAGTAA				Eb_429T.dna
AAACACCACCGCCGGGACC	GCGAACG	AGTCACCCGCCACTGCGTGCTGACT	AAACACCAAAACCAAAAGTAA				Eb_GEBT.dna
500	510	520	530	540	550	560	
ATTGATGTCAGCTGGCGCAACCTG	CCCTTCGTCTCCATTAA	CGATCCGCTGCTGATGATCGGCAA					Eb_429T.dna
ATTGATGTCAGCTGGCGCAACCTG	CCCTTCGTCTCCATTAA	CGATCCGCTGCTGATGATCGGCAA					Eb_GEBT.dna
570	580	590	600	610	620	630	
GCCCGCCGGCTGACCGCC	ACCGGTATGGATGCC	CTGACCCACGGTAGAGGGCCTATAT	CTCCAAA				Eb_429T.dna
GCCCGCCGGCTGACCGCC	ACCGGTATGGATGCC	CTGACCCACGGTAGAGGGCCTATAT	CTCCAAA				Eb_GEBT.dna
640	650	660	670	680	690	700	
GACGCCAACCCGGTTACC	GATGCCCTGCTATT	CAAGGCCATCAAAC	TGCAACCTTGCGCCAGG				Eb_429T.dna
GACGCCAACCCGGTTACC	GATGCCCTGCTATT	CAAGGCCATCAAAC	TGCAACCTTGCGCCAGG				Eb_GEBT.dna
710	720	730	740	750	760	770	
CGTCGCCCTGGGACCAAC	CTCAAAGCCCGTGA	AAACATGGCCTGCGCC	TCTCTGCTGGCCGGGATGGC				Eb_429T.dna
CGTCGCCCTGGGACCAAC	CTCAAAGCCCGTGA	AAACATGGCCTGCGCC	TCTCTGCTGGCCGGGATGGC				Eb_GEBT.dna
780	790	800	810	820	830	840	
CTTAACACGCCAACCTGG	GCTATGTTACGCC	ATGGCTCACCA	CGTGGCGGCC				Eb_429T.dna
CTTAACACGCCAACCTGG	GCTATGTTACGCC	ATGGCTCACCA	CGTGGCGGCC				Eb_GEBT.dna
850	860	870	880	890	900	910	
CACGGGGTGGCGAAC	GC	GGTCTGCCCCATG	TCTGCGCTATAAC	CTGATTGCCAACCCGG	AAAAAT		Eb_429T.dna
CACGGGGTGGCGAAC	GC	GGTCTGCCCCATG	TCTGCGCTATAAC	CTGATTGCCAACCCGG	AAAAAT		Eb_GEBT.dna
920	930	940	950	960	970	980	
TTGCCGATATGCCAC	CTTTATGGGG	AAACACCCACGGCT	TTTCCACCATGGAC	GCAGCGGAGCTGGC			Eb_429T.dna
TTGCCGATATGCCAC	CTTTATGGGG	AAACACCCACGGCT	TTTCCACCATGGAC	GCAGCGGAGCTGGC			Eb_GEBT.dna
990	1000	1010	1020	1030	1040	1050	
CATCAGCGCCATTGCCG	TCTGCTAAAGAT	GTCGGGATCCC	CGACCTGCGTGA	ACTGGGGTAAAA			Eb_429T.dna
CATCAGCGCCATTGCCG	TCTGCTAAAGAT	GTCGGGATCCC	CGACCTGCGTGA	ACTGGGGTAAAA			Eb_GEBT.dna
1060	1070	1080	1090	1100	1110	1120	
GAGGCCGACTTCCC	GATACATGGC	AGAAATGGCC	CTGAAAGACGGCA	ACGCC	TTCTCTA	ACCCGGCGCAAAG	Eb_429T.dna
GAGGCCGACTTCCC	GATACATGGC	AGAAATGGCC	CTGAAAGACGGCA	ACGCC	TTCTCTA	ACCCGGCGCAAAG	Eb_GEBT.dna
1130	1140	1150	1160	1170			
GGAACGAAAAAGAGAT	TGCCGACATTT	CCGCCAGGCATT	TCTGA				Eb_429T.dna
GGAACGAAAAAGAGAT	TGCCGACATTT	CCGCCAGGCATT	TCTGA				Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIGURE 2

10	40	70	100	130	160
10	MSYRMFDYLVPNVNFFGPGAVSVVGQRCQLGGKKALLVTDKGLRAIKDGAVIDQTVKHLK				
10	MSYRMFDYLVPNVNFFGPGAVSVVGQRCQLGGKKALLVTDKGLRAIKDGAVIDQTVKHLK				Eb_429T.dna
190	220	250	280	310	340
190	AAGIEEVVIFDGVEPNPKDTNVLDGLAMFRKEQCDMIIITVGGGSPE				
190	AAGIEEVVIFDGVEPNPKDTNVLDGLAMFRKEQCDMIIITVGGGSPE				Eb_429T.dna
190					Eb_GEBT.dna
370	400	430	460	490	520
370	LYSYAGIETLTNPPLPIIAVNTTAGTASEVTRHCVLTNTKTKVFKFIVSWRNLPVSIN				
370	LYSYAGIETLTNPPLPIIAVNTTAGTASEVTRHCVLTNTKTKVFKFIVSWRNLPVSIN				Eb_429T.dna
370					Eb_GEBT.dna
550	580	610	640	670	700
550	PLLMIGKPAGLTAATGMDALTHAVEAYISKDANPVTDASAIQAIKLIATNLRQAVALGTN				
550	PLLMIGKPAGLTAATGMDALTHAVEAYISKDANPVTDASAIQAIKLIATNLRQAVALGTN				Eb_429T.dna
550					Eb_GEBT.dna
730	760	790	820	850	880
730	ALKARENMACASLLAGMAFNNANLGYVHAMAHQLGGLYDMAHGVANAVLLPHVCRYNLI				
730	ALKARENMACASLLAGMAFNNANLGYVHAMAHQLGGLYDMAHGVANAVLLPHVCRYNLI				Eb_429T.dna
730					Eb_GEBT.dna
910	940	970	1000	1030	1060
910	PEKFADIATFMGENTTGLSTMDDAELAISAIARLSKDVGIPQHLRELGVKEADFPYMAEM				
910	PEKFADIATFMGENTTGLSTMDDAELAISAIARLSKDVGIPQHLRELGVKEADFPYMAEM				Eb_429T.dna
910					Eb_GEBT.dna
1090	1120	1150			
1090	ALKDGNFSNPRKGNEKEIADIFRQAF				
1090	ALKDGNFSNPRKGNEKEIADIFRQAF				Eb_429T.dna
1090					Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIGURE 3

TEMPERATURE

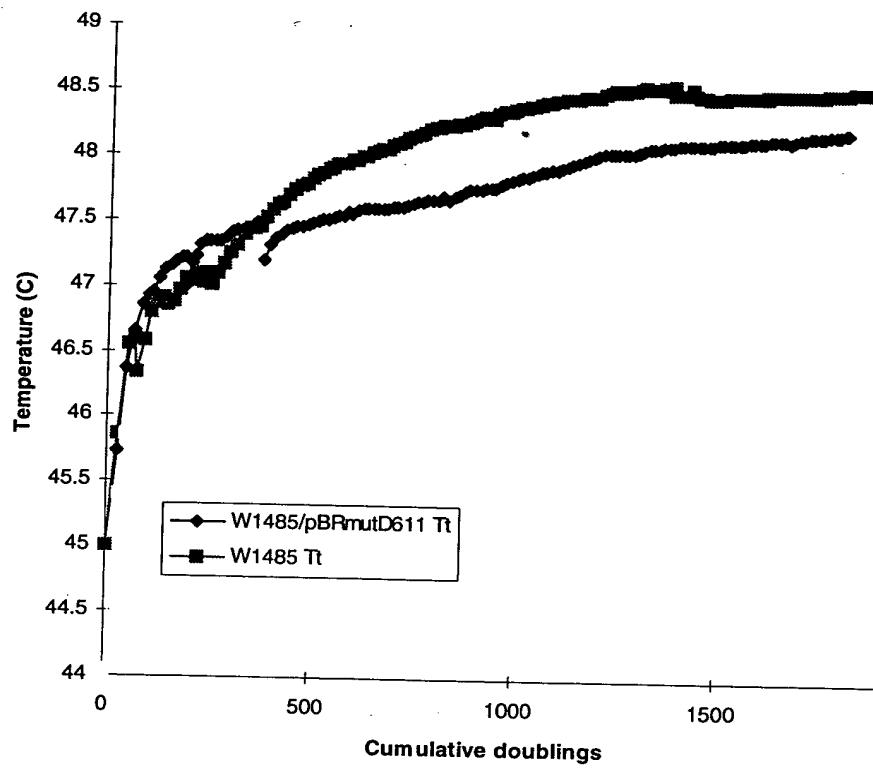


Figure 4

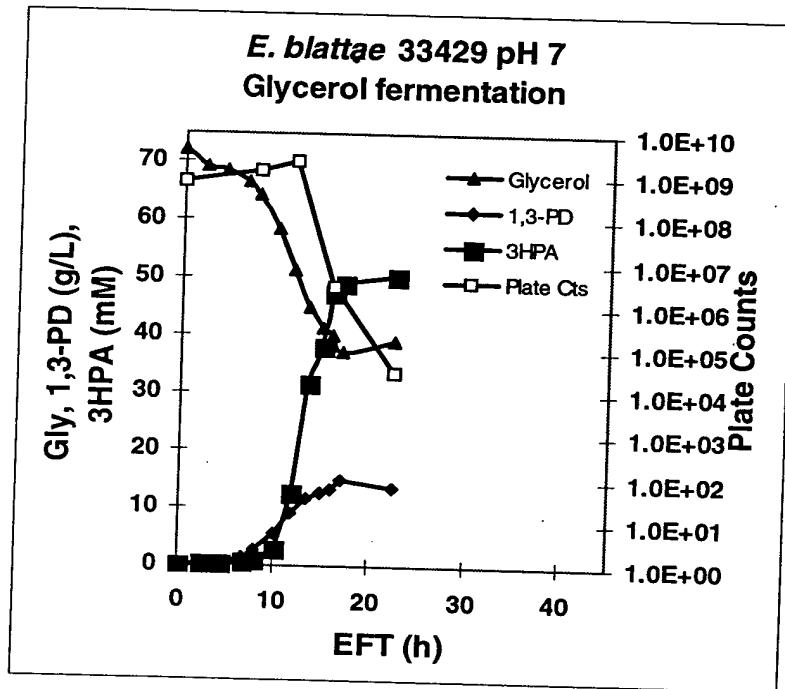


Figure 5

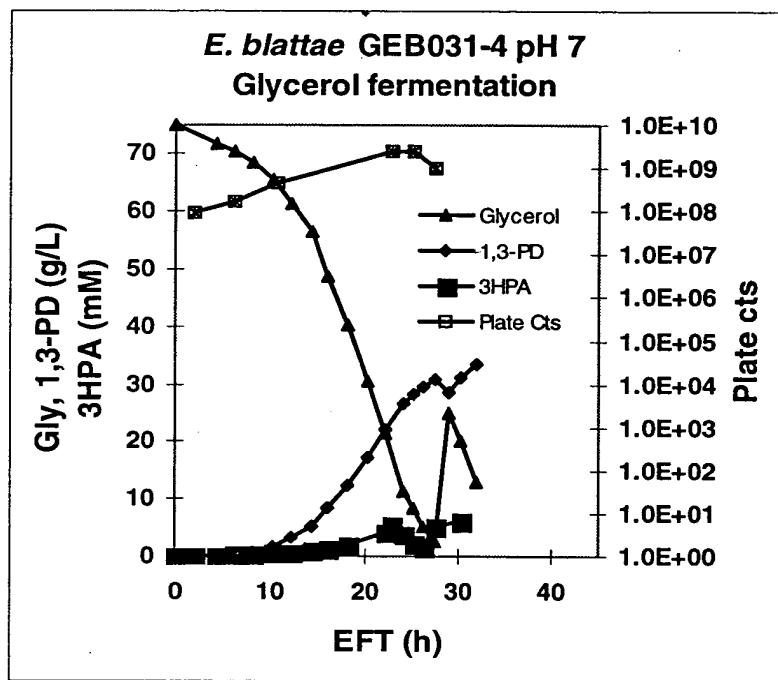


Figure 6